

```

1 MVRSGNKAADVLCMDVGFTMSNSIPGIESPFEQAKKVITMFVQRQVFAEN 50
  |||||
1 MVRSGNKAADVLCMDVGFTMSNSIPGIESPFEQAKKVITMFVQRQVFAEN 50

51 KDEIALVLFGTGTDNPLSGGDQYQNI TVHRHMLPDPFDLLEDIESKIOP 100
  |||||
51 KDEIALVLFGTGTDNPLSGGDQYQNI TVHRHMLPDPFDLLEDIESKIOP 100

101 GSQQADELDALIVSMDVIQHETIGKKFEKRHIEIFTDLSSRFSKSQLDII 150
  |||||
101 GSQQADELDALIVSMDVIQHETIGKKFEKRHIEIFTDLSSRFSKSQLDII 150

151 IHSLKKCDISLQFFLPFSLGKEDGSDRGDGPFRLGGHGSPFPLKGITEQ 200
  |||||
151 IHSLKKCDISLQFFLPFSLGKEDGSDRGDGPFRLGGHGSPFPLKGITEQ 200

201 QKEGLEIVKMVMISLEGEDGLDEIYSFSESLRKL CVFKKIERHSIHWPCR 250
  |||||
201 QKEGLEIVKMVMISLEGEDGLDEIYSFSESLRKL CVFKKIERHSIHWPCR 250

```

Fig. 1

251 LTIGSNLSIRIAAYKSILQERVKKTWTVVDAKTLKKEDIQETVYCLNDD 300
|||||
251 LTIGSNLSIRIAAYKSILQERVKKTWTVVDAKTLKKEDIQETVYCLNDD 300
301 DETEVLKEDI IQFRYGSDI VPF SKVDEEQMKYKSE GKCF SVLGCKSSQ 350
|||||
301 DETEVLKEDI IQFRYGSDI VPF SKVDEEQMKYKSE GKCF SVLGCKSSQ 350
351 VQRRFFMGNOVLKVFAARDDEAAVALSSLIHALDDLDMVAIVRYAYDKR 400
|||||
351 VQRRFFMGNOVLKVFAARDDEAAVALSSLIHALDDLDMVAIVRYAYDKR 400
401 ANPQVGVAFPHIKHNYECLVYVQLPFMEDLRQYMFSSLKNSKKYAPTEAQ 450
|||||
401 ANPQVGVAFPHIKHNYECLVYVQLPFMEDLRQYMFSSLKNSKKYAPTEAQ 450
451 LNAVDALIDMSLAKKDEKDTLEDLFPTTKIPNPRFORLEQ 492
|||||
451 LNAVDALIDMSLAKKDEKDTLEDLFPTTKIPNPRFORLEQ 492

Fig. 1 (Cont.)

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1  MVRSGNKAADVLCMDVGFTMSNSIPGIESPFEOAKKVI TMFVQRQVFAEN 50
  |||||
1  MVRSGNKAADVLCMDVGFTMSNSIPGIESPFEOAKKVI TMFVQRQVFAEN 50

51 KDEIALVLEFGTDGTDNPLSGGDQYQNI TVHRHMLPDEFDLLEDIESKIQP 100
  |||||
51 KDEIALVLEFGTDGTDNPLSGGDQYQNI TVHRHMLPDEFDLLEDIESKIQP 100

101 GSQQADEFLDALIVSMDVIQHETIGKKFEKRRHIEI FTDLSSRFSKSQLDII 150
  |||||
101 GSQQADEFLDALIVSMDVIQHETIGKKFEKRRHIEI FTDLSSRFSKSQLDII 150

151 IHSLKKCDISLOFFLPFSLGKEDGSGDRGDGPFR LGHGHPFPLKGITEQ 200
  |||||
151 IHSLKKCDISLOFFLPFSLGKEDGSGDRGDGPFR LGHGHPFPLKGITEQ 200

201 QKEGLEIVKMVMISLEGEDGLDEIYSFSESLRKL CVFKKIERHSIHWPGR 250
  |||||
201 QKEGLEIVKMVMISLEGEDGLDEIYSFSESLRKL CVFKKIERHSIHWPGR 250

```

Fig. 2.

```

251 LTIGSNLSIRIAAYKSILQERVKKTWTVVDAKTLKKEDIQKETVYCLNDD 300
|||||
251 LTIGSNLSIRIAAYKSILQERVKKTWTVVDAKTLKKEDIQKETVYCLNDD 300
.
301 DETE..... 304
||||
301 DETEVLKEDIQGFYGSDIVPFSKVDEEQMKYKSEKCFSVLGFCKSSQ 350
.
305 .....LNPPAEVTTKSQIPLSKIKTLFPLIEAKKKDQVTA 339
|||||
501 PREPLPPIQQHIWNMLNPPAEVTTKSQIPLSKIKTLFPLIEAKKKDQVTA 550
.
340 QEIFQDNHEDGPTAKKLKTEQGAHFSVSSLAEGSVTSVGSVNPAENFRV 389
|||||
551 QEIFQDNHEDGPTAKKLKTEQGAHFSVSSLAEGSVTSVGSVNPAENFRV 600
.
390 LVKQKKASFEESASNQLINHIEQFLDTNETPYFMKSIDCIRAFREEAIKFS 439
|||||
601 LVKQKKASFEESASNQLINHIEQFLDTNETPYFMKSIDCIRAFREEAIKFS 650

```

Fig. 2 (Cont.)

```

440 EEQRFNNFLKALQEKVEIKQLNHFWEIVVQDGITLITKEEASGSSVTAAE 489
    |||||
651 EEQRFNNFLKALQEKVEIKQLNHFWEIVVQDGITLITKEEASGSSVTAAE 700
    |||||

    490 AKKFLAPKDKPSGDTAAVFEEGGDVDDLDMI 521
        |||||
    701 AKKFLAPKDKPSGDTAAVFEEGGDVDDLDMI 732

```

Fig. 2 (Cont.)

2 GCGCSSHPEDDWMENIDVCENCHYPIVPLDGKGTLLIRNGSEVRDPLVTY 51
 |||||
 1 GCGCSSHPEDDWMENIDVCENCHYPIVPLDGKGTLLIRNGSEVRDPLVTY 50
 52 EGSNPPASPLQDNLVIALHSYEPSHDGDLGFEKGEQLRILEQSGEWWKAQ 101
 |||||
 51 EGSNPPASPLQDNLVIALHSYEPSHDGDLGFEKGEQLRILEQSGEWWKAQ 100
 102 SLTTGQEGFIPNFVAKANSLEPEPWFVKNSRKDAERQLLAPGNTHGSF 151
 |||||
 101 SLTTGQEGFIPNFVAKANSLEPEPWFVKNSRKDAERQLLAPGNTHGSF 150
 152 LIRESETAGSFSLSVRDFDQNGEVVKHYKIRNLDNNGGFYISPRITFPG 201
 |||||
 151 LIRESETAGSFSLSVRDFDQNGEVVKHYKIRNLDNNGGFYISPRITFPG 200
 202 LHELVRHYTNASDGLCTRLSRPCQTQKPQKPWWEDEWEVPRETCLKLVERL 251
 |||||
 201 LHELVRHYTNASDGLCTRLSRPCQTQKPQKPWWEDEWEVPRETCLKLVERL 250

Fig. 3

252 GAGQGEVWMGYNGHTKVAVKS LKQGS MSPDAFLAEANL MKQLQHRLV 301
 |||||
 251 GAGQGEVWMGYNGHTKVAVKS LKQGS MSPDAFLAEANL MKQLQHRLV 300
 |||||
 302 RLYAVVTQEPIYIITEYMENGLVDFL KTPSGIKLTINKLLDMAAQIAEG 351
 |||||
 301 RLYAVVTQEPIYIITEYMENGLVDFL KTPSGIKLTINKLLDMAAQIAEG 350
 |||||
 352 MAFIEERNYIHRDLRAANILVSDTL SCKIADFG LARLIEDIHHQVR 397
 ||||| : |
 351 MAFIEERNYIHRDLRAANILVSDTL SCKIADFG LARLIEDNEYTAR 396

Fig. 3(Cont.)

```

302 TLKLVERLGAGQGEVWMGYNGHTKVAVKSLKQGSMSPD AFLAEANL MK 351
|||||
243 TLKLVERLGAGQGEVWMGYNGHTKVAVKSLKQGSMSPD AFLAEANL MK 292

352 QLQHRLVRLYAVVTOEPIYIITEYMENGLVD FLKTPSGIKLTINKLLD 401
|||||
293 QLQHRLVRLYAVVTOEPIYIITEYMENGLVD FLKTPSGIKLTINKLLD 342

402 MAAQIAEGMAFIEERNYIHRDLRAANILVSDTL SCKIADEGLARLIEDNE 451
|||||
343 MAAQIAEGMAFIEERNYIHRDLRAANILVSDTL SCKIADEGLARLIEDNE 392

452 YTAREGAKFPIKWTAPEAINYGTFTIKSDVW SFGILLTEIVTHGRIPYPG 501
|||||
393 YTAREGAKFPIKWTAPEAINYGTFTIKSDVW SFGILLTEIVTHGRIPYPG 442

502 MTNPEVIQNLERGYRMVRPDNCPEELYQLMR LCKWKEPEDRPTFDYLR SV 551
|||||
443 MTNPEVIQNLERGYRMVRPDNCPEELYQLMR LCKWKEPEDRPTFDYLR SV 492

552 LEDFFTATEGQYQPQ 567
|||||
493 LEDFFTATEGQYQPQ 508

```

Fig. 4 (Cont.)


```

2 GCGSSHPEDDWMENIDVCENCHYPIVPLDGKGTLLIRNGSEVRDPLVTY 51
  |||||
1 GCGSSHPEDDWMENIDVCENCHYPIVPLDGKGTLLIRNGSEVRDPLVTY 50
52 EGSNPPASPLQGDPRQGLKDKACGSLAVGFHLSPTYFLPGLAFLVPHPV 101
  |||||
51 EGSNPPASPLQ..... 61

102 TPGFLPIPARFSLTPLVFTDNLVIALHSYEPSHGDGLGFEKGEQLRILEQ 151
  |||||
62 .....DNLVIALHSYEPSHGDGLGFEKGEQLRILEQ 92

152 SGEWWKAQSLTTGQEGFIPFNFAKANSLPEPEWFFKNLSRKDAERQLLA 201
  |||||
93 SGEWWKAQSLTTGQEGFIPFNFAKANSLPEPEWFFKNLSRKDAERQLLA 142

202 PGNTHGSFLIRESESTAGSFSLSVRDFDQNGEVVKHYKIRNLDNGGFYI 251
  |||||
143 PGNTHGSFLIRESESTAGSFSLSVRDFDQNGEVVKHYKIRNLDNGGFYI 192

252 SPRITFPGLHELVRHYTNASDGLCTRLSRPCQTQKPKPWWEDWEVPRE 301
  |||||
193 SPRITFPGLHELVRHYTNASDGLCTRLSRPCQTQKPKPWWEDWEVPRE 242

```

Fig. 4

```

1  MRIAVICFCLLGITCAIPVKQADSGSSEEKQLYNKYPDATWLNPDPSQ 50
   |||||
1  MRIAVICFCLLGITCAIPVKQADSGSSEEKQLYNKYPDATWLNPDPSQ 50

51  KQLLAPQNAVSEETNDFKQETLPSKSNEHDMDDDEDDDDHVDVSQ 100
   |||||
51  KQLLAPQNAVSEETNDFKQETLPSKSNEHDMDDDEDDDDHVDVSQ 100

101 DSIDSNDSDVDVDDTDDSHQSDSHHSDSEDELVTDFPTDLPATEVFTPVV 150
   |||||
101 DSIDSNDSDVDVDDTDDSHQSDSHHSDSEDELVTDFPTDLPATEVFTPVV 150

151 PTVDITYDGRGDSVYGLRSKSKFRRPDIQVNPLTD 186
   |||||
151 PTVDITYDGRGDSVYGLRSKSKFRRPDIQYPDATD 186

```

Fig. 5


```

1 MRARPQVCEALLFALALQGTVCYGIKWIALSKTPSALALNQTHCKQLEG 50
  |||||
1 MRARPQVCEALLFALALQGTVCYGIKWIALSKTPSALALNQTHCKQLEG 50

51 LVSAQVQLCRSNLELMHTVVHAAREVMKACRRAFADMRWNCSSIELAPNY 100
  |||||
51 LVSAQVQLCRSNLELMHTVVHAAREVMKACRRAFADMRWNCSSIELAPNY 100

101 LLDLERTRESAFVYALSAAISHAIACTSGDLPGCSCGPVGEPPGP 150
  |||||
101 LLDLERTRESAFVYALSAAISHAIACTSGDLPGCSCGPVGEPPGP 150

151 GNRWGRCADNLSYGLLMGAKFSDAPMKVKKTGSQANKLMRLHNSEVGRQA 200
  |||||
151 GNRWGRCADNLSYGLLMGAKFSDAPMKVKKTGSQANKLMRLHNSEVGRQA 200

201 LRASLEMKCKCHGVSGCSIRTCWKGLQELQDVAADLKTRYLSATKVVHR 250
  |||||
201 LRASLEMKCKCHGVSGCSIRTCWKGLQELQDVAADLKTRYLSATKVVHR 250

```

Fig. 7

251 PMGTRKHLVPKDLDIRPVKDSELVYLQSSPFCMKNEKVGSHGTQDRQCN 300
 |||||
 251 PMGTRKHLVPKDLDIRPVKDSELVYLQSSPFCMKNEKVGSHGTQDRQCN 300
 |||||
 301 KTSNGSDSCDLM.....CCYVTCRRCERTVER 327
 |||||
 301 KTSNGSDSCDLMCCGRGYNPYTDRVVERCHCKYHWCCYVTCRRCERTVER 350
 |||||
 328 YVCK 331
 ||||
 351 YVCK 354

Fig. 7 (Cont.)

```

1 MRARPQVCEALLFALALQTGVCYGIKWALSKTPSALALNQTQHCKQLEG 50
  |||||
1 MRARPQVCEALLFALALQTGVCYGIKWALSKTPSALALNQTQHCKQLEG 50
  |||||
1 MRARPQVCEALLFALALQTGVCYGIKWALSKTPSALALNQTQHCKQLEG 50
  |||||
51 LVSAQVQLCRSNLELMHTVVHAAREVMKACRRAFADMRWNCSSIELAPNY 100
  |||||
51 LVSAQVQLCRSNLELMHTVVHAAREVMKACRRAFADMRWNCSSIELAPNY 100
  |||||
101 LLDLERTRESAFVYA..... 116
  |||||
101 LLDLERTRESAFVYALSAAATISHAIARACTSGDLPGCSCGPVGPPEPPGP 150
  |||||
117 .....AADLKTRYLSATKVVHR 133
  |||||
201 LRASLEMKCKCHGVSGSCSIRTCWKGLQELQDVAADLKTRYLSATKVVHR 250
  |||||
134 PMGTRKHLVPKDLDIRPVKDSSELVYLQSSPDFCMKNEKVSGHGTQDRQCN 183
  |||||
251 PMGTRKHLVPKDLDIRPVKDWELVYLQSSPDFCMKNEKVSGHGTQDRQCN 300
  |||||

```

Fig. 8

184 KTSNGSDSCDLMCCGRGYNPYTDRVVERCHCKYHWCCYVTCRRCERTVER 233
|||||
301 KTSNGSDSCDLMCCGRGYNPYTDRVVERCHCKYHWCCYVTCRRCERTVER 350

234 YVCK 237

||||

351 YVCK 354

Fig. 8 (Cont.)

1 MSPFLRIGLSNFDGSCQSCQGEAVNPYCAVLVKEYVESENGQMYIQKKP 50
 |||||
 1 MSPFLRIGLSNFDGSCQSCQGEAVNPYCAVLVKEYVESENGQMYIQKKP 50
 51 TMYPPWDSTFDAHINKGRVMQIIVKGNVDLISSETVELYSLAERCCKNN 100
 |||||
 51 TMYPPWDSTFDAHINKGRVMQIIVKGNVDLISSETVELYSLAERCCKNN 100
 101 GKTEIWLELKPQGRMLMNARYFLEMSDTKDMNEFEFTEGFFALHQRRAIK 150
 |||||
 101 GKTEIWLELKPQGRMLMNARYFLEMSDTKDMNEFEFTEGFFALHQRRAIK 150
 151 QAKVHHVKCHEFTATFFPQPTFCVSCHEFVWGLNKQGYQCRQCNAAIHKK 200
 |||||
 151 QAKVHHVKCHEFTATFFPQPTFCVSCHEFVWGLNKQGYQCRQCNAAIHKK 200
 201 CIDKVIKCTGSAINSRSTMFKERFKIDMPHRFKVYNYKSPTFCEHCGT 250
 |||||
 201 CIDKVIKCTGSAINSRSTMFKERFKIDMPHRFKVYNYKSPTFCEHCGT 250
 251 LLWGLARQGLKCDACGMNVHHRQCQTKVANLCCGINQKLMAEALAMIESTQQ 300
 |||||
 251 LLWGLARQGLKCDACGMNVHHRQCQTKVANLCCGINQKLMAEALAMIESTQQ 300

Fig. 9


```

301 ARCLRDTEQIFREGPVEIGLPCSIKNEARPPCLPTPGKREPQGISWESPL 350
|||||
301 ARCLRDTEQIFREGPVEIGLPCSIKNEARLPCLPTPGKREPQGISWESPL 350

351 DEVDKMCHLPEPELNKERPSLQIKLKIEDFILHKMLGKSGFKVFLAEFK 400
|||||
351 DEVDKMCHLPEPELNKERPSLQIKLKIEDFILHKMLGKSGFKVFLAEFK 400

401 KTNQFFAIKALKKDVVLMDDDVECTMVEKRVLSLAWEHFPLTHMECTFFT 450
|||||
401 KTNQFFAIKALKKDVVLMDDDVECTMVEKRVLSLAWEHFPLTHMECTFFT 450

451 KENLFFVMEYLNCGDLMYHIQSKHFDLSRATFYAAEIIILGLQFLHSGKI 500
|||||
451 KENLFFVMEYLNCGDLMYHIQSKHFDLSRATFYAAEIIILGLQFLHSGKI 500

501 VYRDLKLDNILLDKDGHIKIADFGMCKENMLGDAKTNTFCGTPDYIAPEI 550
|||||
501 VYRDLKLDNILLDKDGHIKIADFGMCKENMLGDAKTNTFCGTPDYIAPEI 550

```

Fig. 9 (Cont.)

```

551 LLGQKYNHSVDWWSFGVLLYEMLIQSPFHGQDEEEELFHSIRMDNPFYPR 600
|||||
551 LLGQKYNHSVDWWSFGVLLYEMLIQSPFHGQDEEEELFHSIRMDNPFYPR 600

601 WLEKEAKDLLVKV 613
|||||
601 WLEKEAKDLLVKL 613

```

Fig. 9(Cont.)

[illegible]

Fig. 10

```

1 MWSWKCLLFWAVLVTATLCTARPSPTLPEQAQPWGAPVEVESFLVHPGDL 50
  |||||
1 MWSWKCLLFWAVLVTATLCTARPSPTLPEQAQPWGAPVEVESFLVHPGDL 50

51 LQLRCRLRDDVQSINWLRDGVQLAESNRTRITGEEVEVQDSVPADSGLYA 100
  |||||
51 LQLRCRLRDDVQSINWLRDGVQLAESNRTRITGEEVEVQDSVPADSGLYA 100

101 CVTSSPSGSDTTYFSVNVSDALPSSDDDDSSSEEKETDNTKPNRMP 150
  |||||
101 CVTSSPSGSDTTYFSVNVSDALPSSDDDDSSSEEKETDNTKPNRMP 150

151 VAPYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPD 200
  |||||
151 VAPYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPD 200

201 HRIGGYKVRyatWSIIMDSVVPsDKGNyTCIVENEyGSINHTYQLDVVER 250
  |||||
201 HRIGGYKVRyatWSIIMDSVVPsDKGNyTCIVENEyGSINHTYQLDVVER 250

251 SPHRPILQAGLPANKTVALGSNVFEFMCKVYSDPQPPIQLKHIEVNGSKI 300
  |||||
251 SPHRPILQAGLPANKTVALGSNVFEFMCKVYSDPQPPIQLKHIEVNGSKI 300

```

Fig. 11

```

301 GPDNLPYVQILKTAGVNTTDKEMEVLHLRNVSEFDAGEYTCLAGNSIGLS 350
|||||
301 GPDNLPYVQILKTAGVNTTDKEMEVLHLRNVSEFDAGEYTCLAGNSIGLS 350

351 HHSAWLTVLEALEERPAMVTSPLYLEIIIIYCTGAFLISCMVGSVIVYKMK 400
|||||
351 HHSAWLTVLEALEERPAMVTSPLYLEIIIIYCTGAFLISCMVGSVIVYKMK 400

401 SGTKKSDFHQSOMAVHKLAKSIPLRRQVTVSADSSASMSNGVLLVRPSRLS 450
|||||
401 SGTKKSDFHQSOMAVHKLAKSIPLRRQVTVSADSSASMSNGVLLVRPSRLS 450

451 SSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEAI GL 500
|||||
451 SSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEAI GL 500

501 DKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKMI GKHKNI INLLGA 550
|||||
501 DKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKMI GKHKNI INLLGA 550

```

Fig. 11 (Cont.)

```

551 CTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQSSKDL 600
|||||
551 CTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQSSKDL 600
|||||
601 VSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDEVNPKIADFGIARDIHH 650
|||||
601 VSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDEVNPKIADFGIARDIHH 650
|||||
651 IDYKKTTNGRLPVKWMPEALEFDRIYTHQSDVWSFGV 688
|||||
651 IDYKKTTNGRLPVKWMPEALEFDRIYTHQSDVWSFGV 688

```

Fig. 11(Cont.)

2 PKRGKKGAVAE D G D E L R T E P E A K K S K T A A K K N D K E A A G E G P A L Y E D P P D Q 51
 |||||
 1 PKRGKKGAVAE D G D E L R T E P E A K K S K T A A K K N D K E A A G E G P A L Y E D P P D Q 50
 .
 52 K T S P S G K P A T L K I C S W N V D G L R A W I K K K G L D W V K E E A P D I L C L Q E T K C S E 101
 |||||
 51 K T S P S G K P A T L K I C S W N V D G L R A W I K K K G L D W V K E E A P D I L C L Q E T K C S E 100
 .
 102 N K L P A E L Q E L P G L S H Q Y W S A P S D K E G Y S G V G L L S R Q C P L K V S Y G I 146
 |||||
 101 N K L P A E L Q E L P G L S H Q Y W S A P S D K E G Y S G V G L L S R Q C P L K V S Y G I G D E E H 150
 .
 147 A Y V P N A G R G L V R L E Y R Q R W D E A F R K F L K G L A S 178
 |||||
 151 D Q E G R V I V A E F D S F V L V T A Y V P N A G R G L V R L E Y R Q R W D E A F R K F L K G L A S 200
 .
 179 R K P L V L C G D L N V A H E E I D L R N P K G N K K N A G F T P Q E R Q G F G E L L Q A V P L A D 228
 |||||
 201 R K P L V L C G D L N V A H E E I D L R N P K G N K K N A G F T P Q E R Q G F G E L L Q A V P L A D 250

Fig. 12

229 SERHLYPNTTPYAYTFWTYMMNARSKNVGWRLDYFLLSHSLLPALCDSKIR 300
|||||

251 SERHLYPNTTPYAYTFWTYMMNARSKNVGWRLDYFLLSHSLLPALCDSKIR 300
|||||

279 SKALGSDHCPITLYLAL 295
|||||

301 SKALGSDHCPITLYLAL 317
|||||

Fig. 12(Cont.)

2	PKRGKKG	VAEDG	DELRTG	KGMKS	ALLPRN	CGGVCH	SLDVRE	PEAKKSK	51	
1	PKRGKKG	VAEDG	DELRT	EPEAKKSK	26	
52	TAAKKN	KEAAGE	PALYED	PPDQKT	SPSGK	PATLKIC	SWNV	DGLRAWIK	101	
27	TAAKKN	KEAAGE	PALYED	PPDQKT	SPSGK	PATLKIC	SWNV	DGLRAWIK	76	
102	KKGLD	WVKEE	APDIL	CLQET	KCSEN	KLPAEL	QELP	GLSHQY	WSPSDKEG	151
77	KKGLD	WVKEE	APDIL	CLQET	KCSEN	KLPAEL	QELP	GLSHQY	WSPSDKEG	126
152	YSGV	GLLSR	QCPLK	VSYGIG	DEEHDQ	EGRVIV	AEFDS	FVLVTAY	VPNAGR	201
127	YSGV	GLLSR	QCPLK	VSYGIG	DEEHDQ	EGRVIV	AEFDS	FVLVTAY	VPNAGR	176
202	GLVR	LEYRQ	RWDEA	FRKFL	KGLASR	KPLVLC	GDNLN	VAAHEE	IDLRNPKGNK	251
177	GLVR	LEYRQ	RWDEA	FRKFL	KGLASR	KPLVLC	GDNLN	VAAHEE	IDLRNPKGNK	226

Fig. 13

252 KNAGFTPQERQGFCELLQAVPLADSEFRHLYPNTPYAYTFWTYMMNARSKN 301
 |||||
 227 KNAGFTPQERQGFCELLQAVPLADSEFRHLYPNTPYAYTFWTYMMNARSKN 276
 302 VGWRLDYFLLSHSLPALCDSKIRSKALGSDHCPIITLYLAL 342
 |||||
 277 VGWRLDYFLLSHSLPALCDSKIRSKALGSDHCPIITLYLAL 317

Fig. 13(Cont.)

1 MFQAAERPQEWAMEGPRDGLKKERLLDDRHSGLDSMKDEEYEQMVKELQ 50
 |||||
 1 MFQAAERPQEWAMEGPRDGLKKERLLDDRHSGLDSMKDEEYEQMVKELQ 50
 |||||
 1 MFQAAERPQEWAMEGPRDGLKKERLLDDRHSGLDSMKDEEYEQMVKELQ 100
 |||||
 51 EIRLEPQEVPRGSEPWKQQLTEDGDSFLHLAIIHEEKALTMVEVIRQVKGD 100
 |||||
 51 EIRLEPQEVPRGSEPWKQQLTEDGDSFLHLAIIHEEKALTMVEVIRQVKGD 150
 |||||
 101 LAFLNFQNNLQQTPHLAVITNQPEIAEALLGAGCDPELDRFRGNTPLHL 150
 |||||
 101 LAFLNFQNNLQQTPHLAVITNQPEIAEALLGAGCDPELDRFRGNTPLHL 200
 |||||
 151 ACEQGCLASVGVLTQSCCTPHLHSILKATNYNGHTCLHLASIHGYLGIVE 200
 |||||
 151 ACEQGCLASVGVLTQSCCTPHLHSILKATNYNGHTCLHLASIHGYLGIVE 250
 |||||
 201 LLVSLGADVNAQEPNCNGRTALHLAVDLQNPDLVSLLLKCGADVNRVTYQG 250
 |||||
 201 LLVSLGADVNAQEPNCNGRTALHLAVDLQNPDLVSLLLKCGADVNRVTYQG 250

Fig. 14

Page 3 of 3

251 YSPYQLTWGRPSTRIQQQLTLENLQMLPESEDEESYDTESEFFTE 300
|||||
251 YSPYQLTWGRPSTRIQQQLTLENLQMLPESEDEESYDTESEFFTE 300

301 DEV 303
||.
301 DEL 303

Fig. 14 (Cont.)

1 MFQAAERPOEWAMEGPKUGLHVA..... 50
1 MFQAAERPOEWAMEGPRDGLKKERLLDDRHSGLDSMKDEEYEQMVKELQ 50
1 MFQAAERPOEWAMEGPRDGLKKERLLDDRHSGLDSMKDEEYEQMVKELQ 100
51 EIRLEPQEVPRGSEPWKQQLTEDGDSFLHLAIIHEEKALTMENVIRQVKGD 100
51 EIRLEPQEVPRGSEPWKQQLTEDGDSFLHLAIIHEEKALTMENVIRQVKGD 150
101 LAFLNFQNNLQQTPLHLAVITNQPEIAEALLGAGCDPELDRFRGNTPLHL 150
101 LAFLNFQNNLQQTPLHLAVITNQPEIAEALLGAGCDPELDRFRGNTPLHL 183
151 ACEQGCLASVGVLTSCTTPHLHSILKATNYNG..... 200
151 ACEQGCLASVGVLTSCTTPHLHSILKATNYNGTCLHLASIHGYLGIVE 200
151 ACEQGCLASVGVLTSCTTPHLHSILKATNYNGTCLHLASIHGYLGIVE 222
184QEPNGRGTALHLAVDLQNPDLVSLLLKCGADVNRVTYQG 250
201 LLVSLGADVNAQEPNGRGTALHLAVDLQNPDLVSLLLKCGADVNRVTYQG 250

Fig. 15

```

223 YSPYQLTWGRPSTRIQQQLGQLTLLENLQMLPESEDEESYDTESEFFTE 272
    |||||
251 YSPYQLTWGRPSTRIQQQLGQLTLLENLQMLPESEDEESYDTESEFFTE 300
    |||||

273 DELPYDDCVFEGGQRLTL 289
    |||||
301 DELPYDDCVFEGGQRLTL 317

```

Fig. 15 (Cont.)

```

1  MAGIFYFALFSCFGICDAVTGSRVYPANEVTLDSRSVQGELGWIASPL 50
   |||||
1  MAGIFYFALFSCFGICDAVTGSRVYPANEVTLDSRSVQGELGWIASPL 50

51  EGGWEEVSIMDEKNTPIRTYQVCNVMPEPSONNWLRTDWTREGAQRVYIE 100
   |||||
51  EGGWEEVSIMDEKNTPIRTYQVCNVMPEPSONNWLRTDWTREGAQRVYIE 100

101 IKFTLRDCNSLPGVMGTCKETFNLYYESDNDKERFIRENFVKIDTIAA 150
   |||||
101 IKFTLRDCNSLPGVMGTCKETFNLYYESDNDKERFIRENFVKIDTIAA 150

151 DESFTQVDIGDRIMKLNTEIRDVGPLSKKGFYLAQDVGACIALVSRVF 200
   |||||
151 DESFTQVDIGDRIMKLNTEIRDVGPLSKKGFYLAQDVGACIALVSRVF 200

201 YKKCPLTVRNLAQFPDITIGADTSSLVEVRGSCVNNSEEKDVPKMYCGAD 250
   |||||
201 YKKCPLTVRNLAQFPDITIGADTSSLVEVRGSCVNNSEEKDVPKMYCGAD 250

251 GEWLVPIGNCLCNAGHEERSGECQACKIGYYKALSTDAKCPPHSV 300
   |||||
251 GEWLVPIGNCLCNAGHEERSGECQACKIGYYKALSTDAKCPPHSV 300

```

Fig. 16

Fig. 16 (Cont.)


```

601 TYEDPNQAVREFAKEIDASCIEKIEKIVGVGEFGEVCSGRLKVP GKREICV 650
|||||
601 TYEDPNQAVREFAKEIDASCIEKIEKIVGVGEFGEVCSGRLKVP GKREICV 650

651 AIKTLKAGYTDKQRRDFLSEASIMQFDHPNIIHLEGVVTKCKPVMIIITE 700
|||||
651 AIKTLKAGYTDKQRRDFLSEASIMQFDHPNIIHLEGVVTKCKPVMIIITE 700

701 YMENGSLDAFLRKNDGRFTVIQLVGMRLRGISGMKYLSDMSYVHRDLAAR 750
|||||
701 YMENGSLDAFLRKNDGRFTVIQLVGMRLRGISGMKYLSDMSYVHRDLAAR 750

751 NILVNSNLVCKVSDFGMSRVLEDDPEAAATTTRGGKIPIRWTAPEDIAARK 800
|||||
751 NILVNSNLVCKVSDFGMSRVLEDDPEAAATTTRGGKIPIRWTAPEDIAARK 800

801 FTSASDVWSYGIWMWEVMSYGERPYWDMSNQD..... 832
|||||
801 FTSASDVWSYGIWMWEVMSYGERPYWDMSNQDVIIKAIIEGYRLPPPMDCP 850

833 .....PNT 835
|||

851 IALHQMLDCWQKERSDRPKFGQIVNMLDKLIRNPNSLKRGTGESSRPNT 900

```

Fig. 16(Cont.)

836 ALLDPSSPEFSVSVGDWLAIKMDRYKDNFTAAAGIILHRAV
 |||||
 901 ALLDPSSPEFSVSVGDWLAIKMDRYKDNFTAAAGYTTLAEVHVHNQED 950
 886 LARIGITAITHQNKILSSVQAMRTQMOMHGRMVPV 921
 |||||
 951 LARIGITAITHQNKILSSVQAMRTQMOMHGRMVPV 986

Fig. 16(Cont.)

```

1 MNDFGIKNMDQVAPVANSYRGTLKRQPAFDTFDGS LFAVFP SLNEEQTLQ 50
  |||||
1 MNDFGIKNMDQVAPVANSYRGTLKRQPAFDTFDGS LFAVFP SLNEEQTLQ 50

51 EVPTGLDSISHDSANCELP LLTPCSKAVMSQALKA TFSGF..... 90
  |||||
51 EVPTGLDSISHDSANCELP LLTPCSKAVMSQALKA TFSGFKKEQRR LGIP 100

91 .....FWATNEFSLVNVLNQRFGMNGQMLCNLGKERFLEL 125
  |||||
101 KNPWLWSEQQVCQWLLWATNEFSLVNVLNQRFGMNGQMLCNLGKERFLEL 150

126 APDFVGDILWEHLEQMIKENQEKTE DQYEENSHLTSVPHWINSNTLGFGT 175
  |||||
151 APDFVGDILWEHLEQMIKENQEKTE DQYEENSHLTSVPHWINSNTLGFGT 200

176 EQAPYGMQTQNYPKGGLDMSMCPASTPSVLSS EQEFQMF PKSLSSVSVT 225
  |||||
201 EQAPYGMQTQNYPKGGLDMSMCPASTPSVLSS EQEFQMF PKSLSSVSVT 250

226 YCSVSQDFPGSNLNLITNNSGTPKDH DSPENGADSFESSDSL LQSWNSQS 275
  |||||
251 YCSVSQDFPGSNLNLITNNSGTPKDH DSPENGADSFESSDSL LQSWNSQS 300

```

Fig. 17

276 SLVDVQRPVSFEFEDDCSCLNKPMTSEFKDYIQERSDPVEQKPVIP 325
 |||||
 301 SLVDVQRPVSFEFEDDCSCLNKPMTSEFKDYIQERSDPVEQKPVIP 350
 |||||
 326 AAVLAGFTGSGPIQLWQFLLLELLSDKSCQSFISWTGDGWEFKLADPDEVA 400
 |||||
 351 AAVLAGFTGSGPIQLWQFLLLELLSDKSCQSFISWTGDGWEFKLADPDEVA 425
 |||||
 376 RRWGKRKNKPKMNYEKLRLYYDKNIIHKTSRKRYVYFVCDLQNL 450
 |||||
 401 RRWGKRKNKPKMNYEKLRLYYDKNIIHKTSRKRYVYFVCDLQNL 444
 |||||
 451 GFTPEELHAILGVQPDTE 469

Fig. 17 (Cont.)

```

1 MAGSAMSSKFFLVALAIFFSFAQVVEANSWWSLGMNPNVQMSEVYIIGA 50
  |||||
1 MAGSAMSSKFFLVALAIFFSFAQVVEANSWWSLGMNPNVQMSEVYIIGA 50

51 QPLCSQLAGLSQGQKKLCHLYQDHMQYIGEGAKTGIKECQYQFRHRRWNC 100
  |||||
51 QPLCSQLAGLSQGQKKLCHLYQDHMQYIGEGAKTGIKECQYQFRHRRWNC 100

101 STVDNTSVFGRVMQIGSRETAFTYAVSAAGVNVNAMSRACTEGELSTCGCS 150
  |||||
101 STVDNTSVFGRVMQIGSRETAFTYAVSAAGVNVNAMSRACTEGELSTCGCS 150

151 RAARPKDLPRDWLWGGCGDNIDYGYRFAKEFVDARERERIHAKGSYESAR 200
  |||||
151 RAARPKDLPRDWLWGGCGDNIDYGYRFAKEFVDARERERIHAKGSYESAR 200

201 ILMNLHNNAGRRTVVYNLADVACKCHGVSGCSLKTCLWLQLADFRKVGDA 250
  |||||
201 ILMNLHNNAGRRTVVYNLADVACKCHGVSGCSLKTCLWLQLADFRKVGDA 250

251 LKEKYDT 257
  |||||
251 LKEKYDS 257

```

Fig. 18

```

1 MALRRSMGRPGLPPLPLPPPPRLGLLLAESAAGLKLMGAPVKLTVSQGQ 50
  |||||
1 MALRRSMGRPGLPPLPLPPPPRLGLLLAESAAGLKLMGAPVKLTVSQGQ 50

51 PVKLNCSEGMEEPDIQWKDGAVVQNLDQLYIPVSEQHWIGFSLKSVE 100
  |||||
51 PVKLNCSEGMEEPDIQWKDGAVVQNLDQLYIPVSEQHWIGFSLKSVE 100

101 RSDAGRYWCQVEDGGETEISQPVWLTVEGVPEFTVEPKDLAVPPNAPFQL 150
  |||||
101 RSDAGRYWCQVEDGGETEISQPVWLTVEGVPEFTVEPKDLAVPPNAPFQL 150

151 SCEAVGPPEPVTIVVWRGTTKIGGPAPSPSVLNVGTQSTMFSCAHNL 200
  |||||
151 SCEAVGPPEPVTIVVWRGTTKIGGPAPSPSVLNVGTQSTMFSCAHNL 200

201 KGLASSRTATVHLQALPAAPFNI TVTKLSSNASVAVWMPGADGRALLQSC 250
  |||||
201 KGLASSRTATVHLQALPAAPFNI TVTKLSSNASVAVWMPGADGRALLQSC 250

251 TVQVTQAPGGWEVLAVVVPVPPFTCLLRDLVPATNYSRLVRRCANALGPSP 300
  |||||
251 TVQVTQAPGGWEVLAVVVPVPPFTCLLRDLVPATNYSRLVRRCANALGPSP 300

```

Fig. 19

301 YADWVPFQTKGLAPASAPQNLHAIRTDGLILEWEEVIPEAPLEGPLGPY 350
 |||||
 301 YADWVPFQTKGLAPASAPQNLHAIRTDGLILEWEEVIPEAPLEGPLGPY 350
 |||||
 301 YADWVPFQTKGLAPASAPQNLHAIRTDGLILEWEEVIPEAPLEGPLGPY 400
 |||||
 351 KLSWVQDNGTQDELTVETRANLTGWDPQKDLIVRVCVSNVAVGCGPWSQP 400
 |||||
 351 KLSWVQDNGTQDELTVETRANLTGWDPQKDLIVRVCVSNVAVGCGPWSQP 400
 |||||
 401 LVSSSHDRAGQQGPPHSRTSWVPVVLGVLTAALALILRRRKET 450
 |||||
 401 LVSSSHDRAGQQGPPHSRTSWVPVVLGVLTAALALILRRRKET 450
 |||||
 451 RFGQAFDSVMARGEPAVHFRAARSFNRPERPERIEATLDSLGSDELKEKL 500
 |||||
 451 RFGQAFDSVMARGEPAVHFRAARSFNRPERPERIEATLDSLGSDELKEKL 500
 |||||
 501 EDVLIPEQQFTLGRMLGKGEFGSVREAQKQEDGSFVKVAVKMLKADIIA 550
 |||||
 501 EDVLIPEQQFTLGRMLGKGEFGSVREAQKQEDGSFVKVAVKMLKADIIA 550
 |||||
 551 SSDIEEFLREAAACMKFEFDHPHVAKLVGVSLRSRAKGRLLPIMVILPFMKH 600
 |||||
 551 SSDIEEFLREAAACMKFEFDHPHVAKLVGVSLRSRAKGRLLPIMVILPFMKH 600

Fig. 19 (Cont.)

601 GDLHAFLLASRIGENPFNLPLQTLIRFMVVDIACGMEYLSRNFIHRDLAA 650
 |||||
 601 GDLHAFLLASRIGENPFNLPLQTLIRFMVVDIACGMEYLSRNFIHRDLAA 650
 651 RNCMLAEDMTVCVADFGLSRKIYSDCRY 678
 |||||
 651 RNCMLAEDMTVCVADFGLSRKIYSGDYY 678

Fig. 19 (Cont.)

Fig. 20

```

301 NGMLRYRIVSQAPSTPSNMFTINNETGDIITVAAGLDREKVQQTLLIQ 350
   |||||
301 NGMLRYRIVSQAPSTPSNMFTINNETGDIITVAAGLDREKVQQTLLIQ 350

   .
351 ATDMEGNPTYGLSNTATAVITVDVNDNPPEFTAMTFYGEVPENRVDIIV 400
   |||||
351 ATDMEGNPTYGLSNTATAVITVDVNDNPPEFTAMTFYGEVPENRVDIIV 400

   .
401 ANLTVTDKQDQHTPAWNAVYRISGGDPTGRFAIQTDPNNSNDGLVTVKPI 450
   |||||
401 ANLTVTDKQDQHTPAWNAVYRISGGDPTGRFAIQTDPNNSNDGLVTVKPI 450

   .
451 DFETNRMFVLTVAAEQVPLAKGIQHPPQSTATVSVTVIDVNENPYFAPN 500
   |||||
451 DFETNRMFVLTVAAEQVPLAKGIQHPPQSTATVSVTVIDVNENPYFAPN 500

   .
501 PKIIRQEEGLHAGTMLTFTTAQDPPDRYMQQNIRYTKLSDPANWLKIDPVN 550
   |||||
501 PKIIRQEEGLHAGTMLTFTTAQDPPDRYMQQNIRYTKLSDPANWLKIDPVN 550

   .
551 GQITTIAVLDRESPNVKNNIYNATFLASDNGIPPMSTGTGLQIYLLDIND 600
   |||||
551 GQITTIAVLDRESPNVKNNIYNATFLASDNGIPPMSTGTGLQIYLLDIND 600

```

Fig. 20 (Cont.)

```

601  NAPQVLPQEAETCETPDPSINITALDYDIDPNAGPFAFDLPLSPVTIKR 650
      |||||
601  NAPQVLPQEAETCETPDPSINITALDYDIDPNAGPFAFDLPLSPVTIKR 650

651  NWTITRLNGDFAQLNLKIKFLEAGIYEVPIIITDSGNPPKSNISILRVKV 700
      |||||
651  NWTITRLNGDFAQLNLKIKFLEAGIYEVPIIITDSGNPPKSNISILRVKV 700

701  CQCDNSGDCSTDVDRIVGAGLGTGAIIAILLCIIILLILVLMFVVMKRRD 750
      |||||
701  CQCDNSGDCSTDVDRIVGAGLGTGAIIAILLCIIILLILVLMFVVMKRRD 750

751  KERQAKQLLIDPEDDVRDNILKYDEEGGGEEDQDYDLSQLQQPD TVEPDA 800
      |||||
751  KERQAKQLLIDPEDDVRDNILKYDEEGGGEEDQDYDLSQLQQPD TVEPDA 800

      801  IKPVGIRRMDERPIHAEPQYPVRSAAAPHGDIGDFINE 838
          |||||
      801  IKPVGIRRMDERPIHAEPQYPVRSAAAPHGDIGDFINE 838

```

Fig. 20 (Cont.)

1 MERVKMINVQRLLEAAEFFLERRECEHGYASSFPMPSPRLQHSKPPRR 50
|||||
1 MERVKMINVQRLLEAAEFFLERRECEHGYASSFPMPSPRLQHSKPPRR 50
51 LSRAQKHSSGSSNTSTANRSTHNELEKNR 79
|||||
51 LSRAQKHSSGTSNTSTANRSTHNELEKNR 79

Fig. 21

```

11 NVQILLEAASYLEQIEKENKCEHGYASSFPMPSPRLQHSKPPRRLSRA 60
   ||| ||| :||. |:||| ||| ||| ||| ||| ||| ||| ||| |||
8 NVQRLLEAAEFLERRERE...CEHGYASSFPMPSPRLQHSKPPRRLSRA 54

61 QKHSSGSSNTSTANRSTHNELEKNRRRAHLRLCLERLKVLIPLGPDCTRHT 110
   ||| |||. ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
55 QKHSSGTSNTSTANRSTHNELEKNRRRAHLRLCLERLKVLIPLGPDCTRHT 104

111 TLGLLNKAKAHIKKLEEAERKSQHOLENLEREQRFLKWRLEQLQGPQEME 160
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
105 TLGLLNKAKAHIKKLEEAERKSQHOLENLEREQRFLKWRLEQLQGPQEME 154

161 RIRMDSIGSTISSDRSDSEREEIEVDVESTEFESHGEVDNISTSIDIDD 210
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
155 RIRMDSIGSTISSDRSDSEREEIEVDVESTEFESHGEVDNISTSIDIDD 204

211 HSSLPSIGSDEGYSSASVKLSFTS 234
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
205 HSSLPSIGSDEGYSSASVKLSFTS 228

```

Fig. 22

251 VWSLGITMIEMAILRFPYESWGTFPQQLKQVVEEPSQLPADRFSPFVD 300
 |||||
 251 VWSLGITMIEMAILRFPYESWGTFPQQLKQVVEEPSQLPADRFSPFVD 300

301 FTAQCLRKKNPAERMSYLELI 320
 |||||
 301 FTAQCLRKKNPAERMSYLEIM 320

Fig. 23(Cont.)

1 MPEIRLRHVVSCSSQDSTHCAENLLKADTYRKWRRAAKAGEKTISVVQLQE 50
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 MPEIRLRHVVSCSSQDSTHCAENLLKADTYRKWRRAAKAGEKTISVVQLQE 50

51 KEEQIHSVDIGNDGSFAFVEVLVGSSAGGAGEQDYEVLLVTSSFMSPPESR 100
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
51 KEEQIHSVDIGNDGSFAFVEVLVGSSAGGAGEQDYEVLLVTSSFMSPPESR 100

101 SGSNPNRVRMFGPDKLVRAAAEKRWDVRKI VCSQPYSKDSPFGLSFVRFH 150
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
101 SGSNPNRVRMFGPDKLVRAAAEKRWDVRKI VCSQPYSKDSPFGLSFVRFH 150

151 SPDPKDEAEAPSQKVTVTKLGQFRVKEEDESANSLRPGALFFSRINKTSP 200
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
151 SPDPKDEAEAPSQKVTVTKLGQFRVKEEDESANSLRPGALFFSRINKTSP 200

201 VTASDPAGPSYAAATLQASSAASSASPVSRAIGSTSKPQESP 242
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
201 VTASDPAGPSYAAATLQASSAASSASPVSRAIGSTSKPQESP 242

Fig. 24

Fig. 25

```

1 MPEIRLRHVSCSSQDSTHCAENLLKADTYRKWRAAKAGEKTISVVLQLE 50
  |||||
1 MPEIRLRHVSCSSQDSTHCAENLLKADTYRKWRAAKAGEKTISVVLQLE 50
  |||||
51 KEEQIHSVDIGNDGSFVEVLVGSSAGGAGEQDYEVLVTSSEMSPESESR 100
  |||||
51 KEEQIHSVDIGNDGSFVEVLVGSSAGGAGEQDYEVLVTSSEMSPESESR 100
  |||||
101 SGSNPNRVRMFGPDKLVRAAAEKRWDVRKIVCSQPYSKDSPFGLSFVRFH 150
  |||||
101 SGSNPNRVRMFGPDKLVRAAAEKRWDVRKIVCSQPYSKDSPFGLSFVRFH 150
  |||||
151 SPDPKDEAEAPSQKVTVTKLGQFRVKEEDESANSLRLEDYMSDRVQFV.. 198
  |||||
151 SPDPKDEAEAPSQKVTVTKLGQFRVKEEDESANSLRPGALFFSRINKTSP 200
  |||||
199 ITAQE.WDPSFEEALMDNPSLA 219
  :|| : ||: | : | |
201 VTASDPAGPSYAAATLQASSAA 222

```

Fig. 26

Fig. 27

301	GEGTEPRRPRAGPEELGKILQGVVVLSGFQNPFRSEL	RDKALELGAKYR	350
301	GEGTEPRRPRAGPEELGKILQGVVVLSGFQNPFRSEL	RDKALELGAKYR	350
351	PDWTRDSTHLICAFANTPKYSQVLGLGGRIVRKEWVLDCHRMRRRLPSRR		400
351	PDWTRDSTHLICAFANTPKYSQVLGLGGRIVRKEWVLDCHRMRRRLPSRR		400
401	YLMAGPGSSSEDEASHSGSGDEAPKLPQKQPQTKTKPTQAAGPSSPQK		450
401	YLMAGPGSSSEDEASHSGSGDEAPKLPQKQPQTKTKPTQAAGPSSPQK		450
451	PPTPEETKAASPVLQEDIDIEGVQSEGQDNGAEDSGDTEDELRRVAEQKE		500
451	PPTPEETKAASPVLQEDIDIEGVQSEGQDNGAEDSGDTEDELRRVAEQKE		500
501	HRLPQGEEENGEDPYAGSTDENTDSEEHQEPDLPVPELPRFLPGQ		546
501	HRLPQGEEENGEDPYAGSTDENTDSEEHQEPDLPVPELPRFFQ GK		546

Fig. 27(Cont.)

1 MAGAIASRMSFS[.]SLKRKQPKTFTVRIVTMDAEME[.]FNCEMKWKGD[.]LDLV 50
 |||||
 1 MAGAIASRMSFS[.]SLKRKQPKTFTVRIVTMDAEME[.]FNCEMKWKGD[.]LDLV 50
 |||||
 51 CRTGLRET[.]WFFGLQYTIKDTVAWLKMDKKVLDH[.]DVSKKEE[.]PVTFHFLAKF 100
 |||||
 51 CRTGLRET[.]WFFGLQYTIKDTVAWLKMDKKVLDH[.]DVSKKEE[.]PVTFHFLAKF 100
 |||||
 101 YPENAEELVQEITQH[.]LF[.]FLQVKKQILD[.]EKIYCPPEASVLLAS[.]YAVQAKY 150
 |||||
 101 YPENAEELVQEITQH[.]LF[.]FLQVKKQILD[.]EKIYCPPEASVLLAS[.]YAVQAKY 150
 |||||
 151 GDYDPSVHKRGFLAQEE[.]LLPKRVINLYQMTPEMWEERI[.]TAWYAEHGRAR 200
 |||||
 151 GDYDPSVHKRGFLAQEE[.]LLPKRVINLYQMTPEMWEERI[.]TAWYAEHGRAR 200
 |||||
 201 DEAEEMEYLKIAQDLEMYGVN[.]YFAIRNKKGT[.]ELLGLGVDALGLHIYDPENRL 250
 |||||
 201 DEAEEMEYLKIAQDLEMYGVN[.]YFAIRNKKGT[.]ELLGLGVDALGLHIYDPENRL 250
 |||||
 251 TPKISFPWKNEIRNISYS[.]DK[.]EFTIKPLDKKIDVFKFNSSKLRVNKLILQL 300
 |||||
 251 TPKISFPW.NEIRNISYS[.]DK[.]EFTIKPLDKKIDVFKFNSSKLRVNKLILQL 299

Fig. 28

301 CIGNHDLFMRRRKADSLVQOMKAQAREEKARK..... 333
 |||||
 300 CIGNHDLFMRRRKADSLVQOMKAQAREEKARKOMERQRLAREKQMREEA 349
 334QMKEEATMANEALMRSEETADLLAEKAQITEEEAKLLA 371
 |||||
 350 ERTRDELERILLQMKEEATMANEALMRSEETADLLAEKAQITEEEAKLLA 399
 372 QKAAEAEQEMQRIKATAIRTEEEKRLMEQKVLAEVLAALKMAEESERRAK 421
 |||||
 400 QKAAEAEQEMQRIKATAIRTEEEKRLMEQKVLAEVLAALKMAEESERRAK 449
 422 EADQLKQDLQEAAREAEERRAKQKLLIATKPTYPNMNPIAPLPPDIPSN 471
 |||||
 450 EADQLKQDLQEAAREAEERRAKQKLLIATKPTYPNMNPIAPLPPDIPSN 499
 472 LIGDSLSEDFKDTDMKRLSMEIEKEKVEYMEKSKHLQEQNLKTEIEAL 521
 |||||
 500 LIGDSLSEDFKDTDMKRLSMEIEKEKVEYMEKSKHLQEQNLKTEIEAL 549
 522 KLKERETALDILHNENSDRGSSKHNTIKKLTQSAKSRVAFFEEEL 567
 |||||
 550 KLKERETALDILHNENSDRGSSKHNTIKKLTQSAKSRVAFFEEEL 595

Fig. 28 (Cont.)

[illegible]

Fig. 29

1 MDLEGRNGGAKKKNFFKLNKSEKDKKEKPTVSFMSFRYSNWLDKLY 50
 |||||
 1 MDLEGRNGGAKKKNFFKLNKSEKDKKEKPTVSFMSFRYSNWLDKLY 50
 51 MVVGTAAIITHGAGLPLMMLVFGEMTDIFANAGNLEDLMSNITNRSND 100
 |||||
 51 MVVGTAAIITHGAGLPLMMLVFGEMTDIFANAGNLEDLMSNITNRSND 100
 101 TGFFMNLEEDMTRYAYYYSGIGAGVLVAAIYQVSFWCLAAGRQIHKIRKQ 150
 |||||
 101 TGFFMNLEEDMTRYAYYYSGIGAGVLVAAIYQVSFWCLAAGRQIHKIRKQ 150
 151 FFHAIMRQEIIGWFDVHDVGELNTRLTDDVSKINEVIGDKIGMFFQSMATF 200
 |||||
 151 FFHAIMRQEIIGWFDVHDVGELNTRLTDDVSKINEVIGDKIGMFFQSMATF 200
 201 FTGFIVGFTTRGWKLTILVILAI SPVLGLSAAVWAKILSSFTDKELLAYAKA 250
 |||||
 201 FTGFIVGFTTRGWKLTILVILAI SPVLGLSAAVWAKILSSFTDKELLAYAKA 250
 251 GAVAAEEVLAAIRTVIAFGGQKKELERYKNLNLEEA KRIGIKKAITANISIG 300
 |||||
 251 GAVAAEEVLAAIRTVIAFGGQKKELERYKNLNLEEA KRIGIKKAITANISIG 300

Fig. 30


```

301 AAFLLIYASYALAFWYGTTLVLSGEYSIGQVLTFFSVLIGAFSVGQASP 350
|||||
301 AAFLLIYASYALAFWYGTTLVLSGEYSIGQVLTFFSVLIGAFSVGQASP 350

351 SIEAFANARGAAYEIFKIIDNKPIDSYSKSGHKPDNIKGNLEFRNVHFS 400
|||||
351 SIEAFANARGAAYEIFKIIDNKPIDSYSKSGHKPDNIKGNLEFRNVHFS 400

401 YPSRKEVKILKGLNLKVQSGQTVALVNSGCCGKSTTVQLMQRLYDPTGEM 450
|||||
401 YPSRKEVKILKGLNLKVQSGQTVALVNSGCCGKSTTVQLMQRLYDPTGEM 450

451 VSDGQDIRTINVRFLREIIGVVSQEPVLEATTIAENIRYGRENVMTDEI 500
|||||
451 VSDGQDIRTINVRFLREIIGVVSQEPVLEATTIAENIRYGRENVMTDEI 500

501 EKAVKEANAYDFIMKLPHKFDTLVGERGAQLSGGQKQRIARALVRNPK 550
|||||
501 EKAVKEANAYDFIMKLPHKFDTLVGERGAQLSGGQKQRIARALVRNPK 550

551 ILLDEATSALDTESEAVVQVALDKARKGRTTIVIAHRLSTVRNADVIAG 600
|||||
551 ILLDEATSALDTESEAVVQVALDKARKGRTTIVIAHRLSTVRNADVIAG 600

```

Fig. 30 (Cont.)

```

601 FDDGVIVEKGNHDELMKEKGIYFKLVMTQAGNEVELENAADESKSEIDA 650
|||||
601 FDDGVIVEKGNHDELMKEKGIYFKLVMTQAGNEVELENAADESKSEIDA 650

651 LEMSSNDSRSSLIRKRSTRRSVRGSAQDRKLSTKEALDESIPVSWRI 700
|||||
651 LEMSSNDSRSSLIRKRSTRRSVRGSAQDRKLSTKEALDESIPVSWRI 700

701 MKLNLTEWPYFVGVFCAIINGGLQPAFAIIFSIIIGVTFTRIDDPETKRQ 750
|||||
701 MKLNLTEWPYFVGVFCAIINGGLQPAFAIIFSIIIGVTFTRIDDPETKRQ 750

751 NSNLSLLELALGIIISFTFFLQGFTEGKAGEILTKRLRYMVFRSMLRQD 800
|||||
751 NSNLSLLELALGIIISFTFFLQGFTEGKAGEILTKRLRYMVFRSMLRQD 800

801 VSWFDDPKNTTGALTTRLANDAAQVKGAIGSRLAVITONIANLGTGIIIS 850
|||||
801 VSWFDDPKNTTGALTTRLANDAAQVKGAIGSRLAVITONIANLGTGIIIS 850

851 FIYGWQLTLLLAIVPIIAIAGVEMKMLSGQALKDKKELEGAGKIATEA 900
|||||
851 FIYGWQLTLLLAIVPIIAIAGVEMKMLSGQALKDKKELEGAGKIATEA 900

```

Fig. 30 (Cont.)

901 IENFRTVVSLTQEQKFEHMYAQSLQVYRNSLRKAHIFGITSFTQAMMY 950
 |||||
 901 IENFRTVVSLTQEQKFEHMYAQSLQVYRNSLRKAHIFGITSFTQAMMY 950
 .
 951 FSYAGCFRFGAYLVAHKIMSFEDVLLVFSVFGAMAVGQVSSFAPDYAK 1000
 |||||
 951 FSYAGCFRFGAYLVAHKIMSFEDVLLVFSVFGAMAVGQVSSFAPDYAK 1000
 .
 1001 AKISAAHIIMIEKTPLIDSYSTEGMLPNTLEGNVTFGEVVFNYPTRPDI 1050
 |||||
 1001 AKISAAHIIMIEKTPLIDSYSTEGMLPNTLEGNVTFGEVVFNYPTRPDI 1050
 .
 1051 PVLQGLSLEVKKGQTLALVGSSGCGKSTVVQLLERYDPLAGKVLLDGKE 1100
 |||||
 1051 PVLQGLSLEVKKGQTLALVGSSGCGKSTVVQLLERYDPLAGKVLLDGKE 1100
 .
 1101 IKRLNVQWLRAHLGIVSQEPILFDCSIAENIAYGDNRSRVVSQEEIVRAAK 1150
 |||||
 1101 IKRLNVQWLRAHLGIVSQEPILFDCSIAENIAYGDNRSRVVSQEEIVRAAK 1150
 .
 1151 EANIHAFTESLPNKYSTKVGDKGTLQSLGGQKQRIARALVRQPHILLD 1200
 |||||
 1151 EANIHAFTESLPNKYSTKVGDKGTLQSLGGQKQRIARALVRQPHILLD 1200

1201	EATSALDTESEKVVQEALDKAREGRTCIVIAHRLSTIQNADLIVVFQNGR	1250
1201	EATSALDTESEKVVQEALDKAREGRTCIVIAHRLSTIQNADLIVVFQNGR	1250
	1251 VKEHGTHQQLLAQKGIYFSMVSVQAGT	1277
	1251 VKEHGTHQQLLAQKGIYFSMVSVQAGT	1277

Fig. 30(Cont.)

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1 MDLEGRNGGAKKKNFFKLNKSEKDKKKKPTVSFMSFRYSNWLDKLY 50
| | | | | | | | | | | | | | | | | | | | | | | | | |
1 MDLEGRNGGAKKKNFFKLNKSEKDKKKKPTVSFMSFRYSNWLDKLY 50

51 MVVGTLAIIHGAGLPLMMLVFGEMLDIFANAGNLEDLMSNITNRSND 100
| | | | | | | | | | | | | | | | | | | | | | | | | |
51 MVVGTLAIIHGAGLPLMMLVFGEMLDIFANAGNLEDLMSNITNRSND 100

101 TGEFMNLEEDMTRYAYYYSGIGAGVLVAAYIQVSFWCLAAGRQIHKIRKQ 150
| | | | | | | | | | | | | | | | | | | | | | | | | |
101 TGEFMNLEEDMTRYAYYYSGIGAGVLVAAYIQVSFWCLAAGRQIHKIRKQ 150

151 FFHAIMRQEIGWFDVHDVGELNTRLTDDVSKINEGIGDKIGMFFQSMATF 200
| | | | | | | | | | | | | | | | | | | | | | | | | |
151 FFHAIMRQEIGWFDVHDVGELNTRLTDDVSKINEVIGDKIGMFFQSMATF 200

201 FTGFIVGFTRGWKLTLVLAISPVLGLSAAVWAKILSSFTDKELLAYAKA 250
| | | | | | | | | | | | | | | | | | | | | | | | | |
201 FTGFIVGFTRGWKLTLVLAISPVLGLSAAVWAKILSSFTDKELLAYAKA 250

251 GAVAEVLAIRTVIAFGGQKKELERYKNLEAKRIGIKKAITANISIG 300
| | | | | | | | | | | | | | | | | | | | | | | | | |
251 GAVAEVLAIRTVIAFGGQKKELERYKNLEAKRIGIKKAITANISIG 300

```

Fig. 31

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301 AAFLLIYASYALAFWYGTTLVLSGEYSIGQVLTFFFSVLIGAFSVGQASP 350
|||||
301 AAFLLIYASYALAFWYGTTLVLSGEYSIGQVLTFFFSVLIGAFSVGQASP 350
|||||

351 SIEAFANARGAAYEIFKIIDNKPSIDSYSGHKGPDNIKGNLEFRNVHFS 400
|||||
351 SIEAFANARGAAYEIFKIIDNKPSIDSYSGHKGPDNIKGNLEFRNVHFS 400
|||||

401 YPSRKEVKILKGLNLKVQSGQTVALVGNSGCGKSTTVQLMQRLYDPTEGM 450
|||||
401 YPSRKEVKILKGLNLKVQSGQTVALVGNSGCGKSTTVQLMQRLYDPTEGM 450
|||||

451 VSVDGGQDIRTINVRFLEIIGVVSQEPVLFATTIAENIRYGRENVMTDEI 500
|||||
451 VSVDGGQDIRTINVRFLEIIGVVSQEPVLFATTIAENIRYGRENVMTDEI 500
|||||

501 EKAVKEANAYDFIMKLPHKFDTLVGERGAQLSGGQKQRIAIARALVRNPK 550
|||||
501 EKAVKEANAYDFIMKLPHKFDTLVGERGAQLSGGQKQRIAIARALVRNPK 550
|||||

551 ILLLDEATSALDTESEAEVQAALDKVSR 578
|||||
551 ILLLDEATSALDTESEAVVQVALDKARK 578

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Fig. 31(Cont.)

1 MSRSKRDNNFYSVEIGDSTFTVLKRYQNLKPIGSAQGIVCAAYDAILER 50
| | | | | | | | | | | | | | | | | | | | | | | | | |
1 MSRSKRDNNFYSVEIGDSTFTVLKRYQNLKPIGSAQGIVCAAYDAILER 50

51 NVAIKKLSRPFQNQTHAKRAYRELVMKC VNHNKI IGLLNVFTPQSLEE 100
| | | | | | | | | | | | | | | | | | | | | | | | | |
51 NVAIKKLSRPFQNQTHAKRAYRELVMKC VNHNKI IGLLNVFTPQSLEE 100

101 FQDVYI VMELMDANLCQVIQMELDHHERMSYLLYQMLCGIKHLHSAGIIHR 150
| | | | | | | | | | | | | | | | | | | | | | | | | |
101 FQDVYI VMELMDANLCQVIQMELDHHERMSYLLYQMLCGIKHLHSAGIIHR 150

151 DLKPSNIVVKSDCTLKILDFGLARTAGTSFMMTPYVVTRYRAPEVILGM 200
| | | | | | | | | | | | | | | | | | | | | | | | | |
151 DLKPSNIVVKSDCTLKILDFGLARTAGTSFMMTPYVVTRYRAPEVILGM 200

201 GYKENTE 207
| | | | :
201 GYKENVD 207

Fig. 32

1 MSRSKRDNNFYSVEIGDSTFTVLKRYQNLKPIGSGAQGIVCAAYDAILER 50
 |||||
 1 MSRSKRDNNFYSVEIGDSTFTVLKRYQNLKPIGSGAQGIVCAAYDAILER 50

51 NVAIKKLSRPFQNOHAKRAYRELVLKMCVNHKNIIGLLNVFTPPQKSLEE 100
 |||||
 51 NVAIKKLSRPFQNOHAKRAYRELVLKMCVNHKNIIGLLNVFTPPQKSLEE 100

101 FQDVYIVMELMDANLCQVIQMELDHERMSYLLYQMLCGIKHLHSAGIIHR 150
 |||||
 101 FQDVYIVMELMDANLCQVIQMELDHERMSYLLYQMLCGIKHLHSAGIIHR 150

151 DLKPSNIVVKS DCTLKILDFGLARTAGTSEMMTPYVVTRYRAPEVILGM 200
 |||||
 151 DLKPSNIVVKS DCTLKILDFGLARTAGTSEMMTPYVVTRYRAPEVILGM 200

201 GYKENVDLWSVGCIMGEMVCHKILFPGRDYIDQWNKVIEQLGTPCPEFMK 250
 |||||
 201 GYKENVDLWSVGCIMGEMVCHKILFPGRDYIDQWNKVIEQLGTPCPEFMK 250

251 KLQPTVRTYVENRPPKYAGYSFEKLFPPDVLFPADSEHNKLLKASQ 293
 |||||
 251 KLQPTVRTYVENRPPKYAGYSFEKLFPPDVLFPADSEHNKLLKASQ 293

Fig. 33

Fig. 34

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251 KLQPTVRTYVENRPPKYAGYSFEKLPDVLFPADSEHNKCLKASQARDLLSK 300
|||||
251 KLQPTVRTYVENRPPKYAGYSFEKLPDVLFPADSEHNKCLKASQARDLLSK 300

301 MLVIDASKRISVDEALQHPYINVWYDPSEAEARSCKL 337
|||||
301 MLVIDASKRISVDEALQHPYINVWYDPSEAEAPPKI 337

```

Fig. 34(Cont.)

7 arsgfyrqevtktawevravryrdlqpvgsgaygavcsavdgrtgakvaik 56
 |||||
 1 ARSGFYRQEVTKTAWEVRAVRYRDLQPVGSGAYGAVCSAVDGRGTGAKVAIK 50
 57 klyrpfqsselfakrayrelrlklkhrhenviglldvftpdetlddftdfy 106
 |||||
 51 KLYRPFQSELF AKRAYRELRLKLKMRHENVIGLLDVFTPDETLDDFTDFY 100
 107 lvmpfmgtldgklmkheklgedriqlvyqmlkglyrihaagiihrdlkp 156
 |||||
 101 LVMPFMGTDLGKLMKHEKLGEDRIQLVYQMLKGLRYIHAAGIIHR.VSP 149
 157 gnlavne 163
 |||
 150 GGEAAHQ 156

Fig. 35

```

1 MSPFLRIGLSNFDGSCQSCQGEAVNPYCAVLVKEYVESENGQMYIQKKP 50
  |||||
1 MSPFLRIGLSNFDGSCQSCQGEAVNPYCAVLVKEYVESENGQMYIQKKP 50

51 TYPPEWDSTFDAHINKGRVMQIIIVKGKNVDLISSETVELYSLAERCERN 100
  |||||
51 TYPPEWDSTFDAHINKGRVMQIIIVKGKNVDLISSETVELYSLAERCERN 100

101 GKTEIWLELKPQGRMLMNARYFLEMSDTKDMNEFEFTEGFFALHQRRAIK 150
  |||||
101 GKTEIWLELKPQGRMLMNARYFLEMSDTKDMNEFEFTEGFFALHQRRAIK 150

151 QAKVHHVKCHEFTATFFPQPTFCVCHFEVWGLNKQGYQCRQCNAAIHKK 200
  |||||
151 QAKVHHVKCHEFTATFFPQPTFCVCHFEVWGLNKQGYQCRQCNAAIHKK 200

201 CIDKVIKCTGSAINSETMFHKERFKIDMPHRFKVYNYKSPTFCEHCGT 250
  |||||
201 CIDKVIKCTGSAINSETMFHKERFKIDMPHRFKVYNYKSPTFCEHCGT 250

```

Fig. 36

```

251 LLWGLARQGLKCDACGMNVHRCQTKVANLCGINQKLMAEALAMISTQQ 300
|||||
251 LLWGLARQGLKCDACGMNVHRCQTKVANLCGINQKLMAEALAMISTQQ 300

301 ARCLRDTEQIFREGPVEIGLPCSIKNEARPPCLPTPGKREPQGISWESPL 350
|||||
301 ARCLRDTEQIFREGPVEIGLPCSIKNEARLPCLPTPGKREPQGISWESPL 350

351 DEVDKMCHLPEPELNKERPSLQIKLKIEDFILHKMLGKSGFKVFLAEFK 400
|||||
351 DEVDKMCHLPEPELNKERPSLQIKLKIEDFILHKMLGKSGFKVFLAEFK 400

401 KTNQFFAIKALKKDVVLMDDDDVECTMVEKRVLSLAWEHFPLTHMECTFTQT 450
|||||
401 KTNQFFAIKALKKDVVLMDDDDVECTMVEKRVLSLAWEHFPLTHMECTFTQT 450

451 KENLFFVMEYLNCGDLMYHIQSCHKFDLSRATFYAAEIIILGLQFLHSGKI 500
|||||
451 KENLFFVMEYLNCGDLMYHIQSCHKFDLSRATFYAAEIIILGLQFLHSGKI 500

```

Fig. 36 (Cont.)

501 VYRDLKLDNILLDKDGHIKIADFGMCKENMLGDAKTNTFCGTPDYIAPEI 550
 |||||
 501 VYRDLKLDNILLDKDGHIKIADFGMCKENMLGDAKTNTFCGTPDYIAPEI 550

 551 LLGQKYNHSVDWWSFGVLLYEMLIQSPFHGQDEEEELFHSIRMDNPFYPR 600
 |||||
 551 LLGQKYNHSVDWWSFGVLLYEMLIQSPFHGQDEEEELFHSIRMDNPFYPR 600

 601 WLEKEAKDLLVK..VRSEAKSVFIR 623
 |||||
 601 WLEKEAKDLLVKLFVREPEKRLGVR 625

Fig. 36 (Cont.)